SCORE Search Results Details for Application 10714389 and Search Result 20070807_102030_us-10-714-389-52.sl.rng.

This page gives you Search Results detail for the Application 10714389 and Search Result 20070807_102030_us-10-714-389-52.sl.rng.

```
                        GenCore version 6.2.1
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```

10/714,389 (handwritten)

```
OM nucleic - nucleic search, using sw model

Run on:          August  8, 2007, 10:13:07 ; Search time 444 Seconds
                                            (without alignments)
                                            6325.687 Million cell updates/sec

Title:           US-10-714-389-52
Perfect score:   379
Sequence:        1 actttgccaagcagtaaagg..........ttcaggtatgagtccagggt 379

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters:      4

Minimum DB seq length: 20
Maximum DB seq length: 379

Post-processing: Minimum Score over Length 100%
                 Listing first 100 summaries

Database :       N_Geneseq_200701:*
                 1:   geneseqn1980s:*
                 2:   geneseqn1990s:*
                 3:   geneseqn2000s:*
                 4:   geneseqn2001as:*
                 5:   geneseqn2001bs:*
                 6:   geneseqn2002as:*
                 7:   geneseqn2002bs:*
                 8:   geneseqn2003as:*
                 9:   geneseqn2003bs:*
                 10:  geneseqn2003cs:*
                 11:  geneseqn2003ds:*
                 12:  geneseqn2004as:*
                 13:  geneseqn2004bs:* .
                 14:  geneseqn2005s:*
                 15:  geneseqn2006s:*
                 16:  geneseqn2007s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Score over Length	% Query Match	Length	DB	ID	Description
1	379	100.0	100.0	379	4	AAH55527	Aah55527 Hu
2	379	100.0	100.0	379	7	ADU01271	Adu01271 Br
3	379	100.0	100.0	379	7	ADZ41535	Adz41535 Hu
4	379	100.0	100.0	379	12	ADN40297	Adn40297 Hu

ALIGNMENTS

RESULT 1
AAH55527
ID   AAH55527 standard; DNA; 379 BP.
XX
AC   AAH55527;
XX
DT   04-SEP-2001 (first entry)
XX
DE   Human breast tumour protein contig 11 DNA sequence.
XX
KW   Cytostatic; vaccine; human; breast tumour protein; breast cancer;
KW   gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200140269-A2.
XX
PD   07-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US032520.
XX
PR   30-NOV-1999;   99US-00451651.
PR   22-FEB-2000; 2000US-00510662.
PR   10-MAR-2000; 2000US-00523586.
PR   07-APR-2000; 2000US-00545068.
PR   15-MAY-2000; 2000US-00571025.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
XX
DR   WPI; 2001-356154/37.
XX
PT   Breast tumor polypeptides and the nucleic acids that encode them, useful
PT   for the prevention, diagnosis and treatment of breast cancer.
XX
PS   Claim 24; Page 139; 221pp; English.
XX
CC   The present sequence is a human breast tumour protein coding sequence.
CC   This sequence may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the breast tumour
CC   protein e.g. breast cancer. For example, this sequence may be used to

SCORE Search Results Details for Application 10714389 and Search Result 20070807_102031_us-10-714-389-52.sl.rge.

Score Home Page   Retrieve Application List   SCORE System Overview   SCORE FAQ   Comments / Suggestions

This page gives you Search Results detail for the Application 10714389 and Search Result 20070807_102031_us-10-714-389-52.sl.rge.

Go Back to previous page

```
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OM nucleic - nucleic search, using sw model

Run on:          August  8, 2007, 10:47:25 ; Search time 2785 Seconds
                                             (without alignments)
                                             9406.317 Million cell updates/sec

Title:           US-10-714-389-52
Perfect score:   379
Sequence:        1 actttgccaagcagtaaagg..........ttcaggtatgagtccagggt 379

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters:      2

Minimum DB seq length: 20
Maximum DB seq length: 379

Post-processing: Minimum Score over Length 100%
                 Listing first 100 summaries

Database :       GenEmbl:*
                 1:  gb_env:*
                 2:  gb_pat:*
                 3:  gb_ph:*
                 4:  gb_pl:*
                 5:  gb_pr:*
                 6:  gb_ro:*
                 7:  gb_sts:*
                 8:  gb_sy:*
                 9:  gb_un:*
                 10:  gb_vi:*
                 11:  gb_ov:*
                 12:  gb_htg:*
                 13:  gb_in:*
                 14:  gb_om:*
                 15:  gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

```
                                      SUMMARIES
                   Score    %
Result            over   Query
   No.   Score  Length  Match Length DB  ID                    Description
-------------------------------------------------------------------------------
    1     379   100.0   100.0    379  2  CS110385              CS110385 Se
    2     379   100.0   100.0    379  2  AX156195              AX156195 Se
```

ALIGNMENTS

```
RESULT 1
CS110385
LOCUS       CS110385                  379 bp    DNA      linear   PAT 22-JUN-2005
DEFINITION  Sequence 52 from Patent WO2005051990.
ACCESSION   CS110385
VERSION     CS110385.1  GI:68148583
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dillon,D.C. and Jiang,Y.
  TITLE     Compositions and methods for the therapy and diagnosis of breast
            cancer
  JOURNAL   Patent: WO 2005051990-A 52 09-JUN-2005;
            Corixa Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .379
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match         100.0%;  Score 379;  DB 2;  Length 379;
  Score over Length   100.0%;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-109;
  Matches  379;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1 ACTTTGCCAAGCAGTAAAGGATCCAGGAGATAGCACTGGATGTGGTGTCATGTCCTGCAA 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ACTTTGCCAAGCAGTAAAGGATCCAGGAGATAGCACTGGATGTGGTGTCATGTCCTGCAA 60

Qy       61 ACATGAACGTTTTCACTTCAGCCTGGAGATCTGCTTCAGAGAAATCTTTGGTGTTTTCGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ACATGAACGTTTTCACTTCAGCCTGGAGATCTGCTTCAGAGAAATCTTTGGTGTTTTCGC 120

Qy      121 TTTTGGCACTCAAAAGTATGTCCAGAAAATCCCAGCGCCTTTTCTGAGTAGTATCTTGTT 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TTTTGGCACTCAAAAGTATGTCCAGAAAATCCCAGCGCCTTTTCTGAGTAGTATCTTGTT 180

Qy      181 TTAGCTTATCCTTAAGAGACTCCTTCCGGTCCTGGATTACTTTCTCTGTGAACTGATGAA 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TTAGCTTATCCTTAAGAGACTCCTTCCGGTCCTGGATTACTTTCTCTGTGAACTGATGAA 240
```

SCORE Search Results Details for Application 10714389 and Search Result 20070807_102033_us-10-714-389-52.sl.rst.

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```
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OM nucleic - nucleic search, using sw model

Run on:          August  8, 2007, 10:49:12 ; Search time 4854 Seconds
                                             (without alignments)
                                             4844.159 Million cell updates/sec

Title:           US-10-714-389-52
Perfect score:   379
Sequence:        1 actttgccaagcagtaaagg..........ttcaggtatgagtccagggt 379

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters:        0

Minimum DB seq length: 20
Maximum DB seq length: 379

Post-processing: Minimum Score over Length 100%
                 Listing first 100 summaries

Database :       EST:*
                 1:   gb_est1:*
                 2:   gb_est3:*
                 3:   gb_est4:*
                 4:   gb_est5:*
                 5:   gb_est6:*
                 6:   gb_htc:*
                 7:   gb_est2:*
                 8:   gb_est7:*
                 9:   gb_est8:*
                 10:  gb_est9:*
                 11:  gb_est13:*
                 12:  gb_est12:*
                 13:  gb_est11:*
                 14:  gb_est10:*
                 15:  gb_gss1:*
                 16:  gb_gss2:*
```

```
                     17:   gb_gss3:*
                     18:   gb_gss4:*
                     19:   gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
                   Score    %
        Result     over    Query
          No.   Score Length Match Length DB   ID                    Description
        -----------------------------------------------------------------------

        No matches found


        Search completed: August  8, 2007, 12:10:19
        Job time : 4854 secs
```

SCORE 3.0   BuildDate: 10/17/2007

SCORE Search Results Details for Application 10714389 and Search Result 20070807_102035_us-10-714-389-52.sl.rni.

This page gives you Search Results detail for the Application 10714389 and Search Result 20070807_102035_us-10-714-389-52.sl.rni.

```
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OM nucleic - nucleic search, using sw model

Run on:         August  8, 2007, 11:20:44 ; Search time 235 Seconds
                                            (without alignments)
                                            5827.613 Million cell updates/sec

Title:          US-10-714-389-52
Perfect score:  379
Sequence:       1 actttgccaagcagtaaagg..........ttcaggtatgagtccagggt 379

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2773932 seqs, 1806713642 residues

Total number of hits satisfying chosen parameters:      0

Minimum DB seq length: 20
Maximum DB seq length: 379

Post-processing: Minimum Score over Length 100%
                 Listing first 100 summaries

Database :      Issued_Patents_NA:*
                1:  /EMC_Celerra_SIDS3/ptodata/1/ina/1_COMB.seq:*
                2:  /EMC_Celerra_SIDS3/ptodata/1/ina/5_COMB.seq:*
                3:  /EMC_Celerra_SIDS3/ptodata/1/ina/6A_COMB.seq:*
                4:  /EMC_Celerra_SIDS3/ptodata/1/ina/6B_COMB.seq:*
                5:  /EMC_Celerra_SIDS3/ptodata/1/ina/7_COMB.seq:*
                6:  /EMC_Celerra_SIDS3/ptodata/1/ina/H_COMB.seq:*
                7:  /EMC_Celerra_SIDS3/ptodata/1/ina/PCTUS_COMB.seq:*
                8:  /EMC_Celerra_SIDS3/ptodata/1/ina/PP_COMB.seq:*
                9:  /EMC_Celerra_SIDS3/ptodata/1/ina/RE_COMB.seq:*
                10:  /EMC_Celerra_SIDS3/ptodata/1/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
```

```
                  Score    %
Result            over   Query
  No.    Score Length  Match Length DB  ID                              Description
------------------------------------------------------------------------------------

No matches found


Search completed: August  8, 2007, 16:33:11
Job time : 235 secs
```

SCORE 3.0   BuildDate: 10/17/2007

SCORE Search Results Details for Application 10714389 and Search Result 20070807_102038_us-10-714-389-52.sl.rnpbm.

This page gives you Search Results detail for the Application 10714389 and Search Result 20070807_102038_us-10-714-389-52.sl.rnpbm.

```
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OM nucleic - nucleic search, using sw model

Run on:          August  8, 2007, 11:32:35 ; Search time 929 Seconds
                                     (without alignments)
                                     5012.932 Million cell updates/sec

Title:           US-10-714-389-52
Perfect score:   379
Sequence:        1 actttgccaagcagtaaagg..........ttcaggtatgagtccagggt 379

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      5

Minimum DB seq length: 20
Maximum DB seq length: 379

Post-processing: Minimum Score over Length 100%
                 Listing first 100 summaries

Database :       Published_Applications_NA_Main:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 11:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 12:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 13:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 14:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                 15:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                 16:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
              Score   %
Result   over   Query
  No.   Score Length Match Length DB ID   Description
----
    1   379 100.0   100.0   379 3 US-09-778-320-52   Sequence 5
    2   379 100.0   100.0   379 3 US-09-910-689-52   Sequence 5
    3   379 100.0   100.0   379 6 US-10-010-742-52   Sequence 5
    4   379 100.0   100.0   379 8 US-10-714-389-52   Sequence 5
    5   379 100.0   100.0   379 8 US-10-717-296-52   Sequence 5

                              ALIGNMENTS

RESULT 1
US-09-778-320-52
; Sequence 52, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, TongTong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-778-320-52

   Query Match   100.0%;   Score 379; DB 3; Length 379;
   Score over Length   100.0%;
   Best Local Similarity 100.0%; Pred. No. 8.3e-104;
   Matches 379; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ACTTTGCCAAGCAGTAAAGGATCCAGGAGATAGCACTGGATGTGGTGTCATGTCCTGCAA 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACTTTGCCAAGCAGTAAAGGATCCAGGAGATAGCACTGGATGTGGTGTCATGTCCTGCAA 60

Qy   61 ACATGAACGTTTTCACTTCAGCCTGGAGATCTGCTTCAGAGAAATCTTTGGTGTTTTCGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ACATGAACGTTTTCACTTCAGCCTGGAGATCTGCTTCAGAGAAATCTTTGGTGTTTTCGC 120

Qy   121 TTTTGGCACTCAAAAGTATGTCCAGAAAATCCCAGCGCCTTTTCTGAGTAGTATCTTGTT 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTTTGGCACTCAAAAGTATGTCCAGAAAATCCCAGCGCCTTTTCTGAGTAGTATCTTGTT 180

SCORE Search Results Details for Application 10714389 and Search Result 20070807_102040_us-10-714-389-52.sl.rnpbn

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions

This page gives you Search Results detail for the Application 10714389 and Search Result 20070807_102040_us-10-714-389-52.sl.rnpbn.

Go Back to previous

```
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OM nucleic - nucleic search, using sw model        ι

Run on:        August  8, 2007, 11:34:20 ; Search time 1211 Seconds
                                          (without alignments)
                                          3373.664 Million cell updates/sec

Title:         US-10-714-389-52
Perfect score: 379
Sequence:      1 actttgccaagcagtaaagg..........ttcaggtatgagtccagggt 379

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      16529674 seqs, 5389851713 residues

Total number of hits satisfying chosen parameters:      3

Minimum DB seq length: 20
Maximum DB seq length: 379

Post-processing: Minimum Score over Length 100%
                 Listing first 100 summaries

Database :     Published_Applications_NA_New:*
         1:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
         2:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
         3:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
         4:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
         5:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
         6:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
         7:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
         8:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
         9:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
        10:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq4:*
        11:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq5:*
        12:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq6:*
        13:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
        14:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
        15:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
        16:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
```

```
17:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
18:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
19:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq6:*
20:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq7:*
21:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq8:*
22:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Score over Length	% Query Match	Length	DB	ID	Description
c 1	32	100.0	8.4	32	6	US-10-535-164-282627	Sequence 2
c 2	32	100.0	8.4	32	11	US-10-536-560-79632	Sequence 7
c 3	32	100.0	8.4	32	11	US-10-536-560-186809	Sequence 1

ALIGNMENTS

RESULT 1
US-10-535-164-282627/c
; Sequence 282627, Application US/10535164
; Publication No. US20070134655A1
; GENERAL INFORMATION:
; APPLICANT: BENTWICH, ITZHAK
; TITLE OF INVENTION: Bioinformatically detectable of Novel Regulatory genes and ther
; FILE REFERENCE: 050992.0200.PCUS13
; CURRENT APPLICATION NUMBER: US/10/535,164
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 548156
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 282627
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Human
US-10-535-164-282627

   Query Match   8.4%;   Score 32; DB 6; Length 32;
   Score over Length   100.0%;
   Best Local Similarity 100.0%; Pred. No. 1.5e+02;
   Matches   32; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   86 GAGATCTGCTTCAGAGAAATCTTTGGTGTTTT 117
            ||||||||||||||||||||||||||||||||
Db   32 GAGATCTGCTTCAGAGAAATCTTTGGTGTTTT 1

RESULT 2
US-10-536-560-79632/c
; Sequence 79632, Application US/10536560
; Publication No. US20060257851A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 06087.0300.PCUS13

BLAST Basic Local Alignment Search Tool

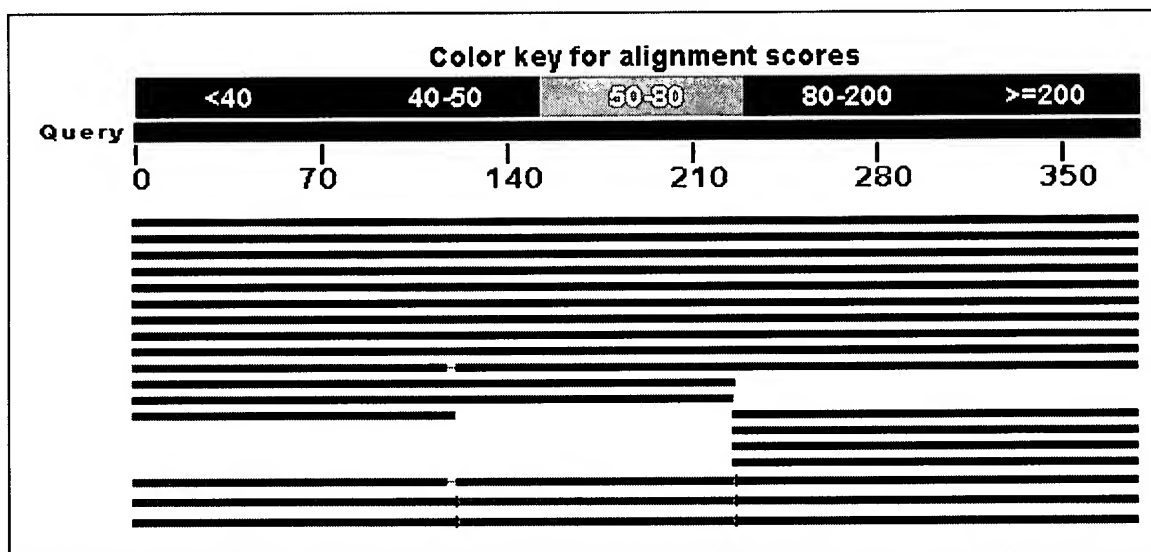**Job Title: lcl|20482 (379 letters)**

-
-
-

10/714, 389

BLASTN 2.2.17 (Aug-26-2007)

RID: M3HBZVH3013 **Database**: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences) 6,093,374 sequences; 22,195,605,443 total letters

Query= Length=379

Distribution of 27 Blast Hits on the Query Sequence

Distance tree of results NEW

Legend for links to other resources: U UniGene E GEO G Gene S Structure □

Sequences producing significant alignments:
(Click headers to sort columns)

AK292175.1	Homo sapiens cDNA FLJ75783 complete cds, highly similar to Homo sapiens cytochrome P450, family 4, subfamily Z, polypeptide 1 (CYP4Z1), mRNA	701	701	100%	0.0	100%	G
XM_BC146466.1	Synthetic construct Homo sapiens clone IMAGE:100015013, MGC:180176 cytochrome P450, family 4, subfamily Z, polypeptide 1 (CYP4Z1) mRNA, encodes complete protein	701	701	100%	0.0	100%	G
BC140382.1	Synthetic construct Homo sapiens clone IMAGE:100014401, MGC:173152 cytochrome P450, family 4, subfamily Z, polypeptide 1 (CYP4Z1) mRNA, encodes complete protein	701	701	100%	0.0	100%	G
AY262056.1	Homo sapiens cytochrome P450 (CYP4Z1) mRNA, complete cds	701	701	100%	0.0	100%	U G
AY358631.1	Homo sapiens clone DNA125150 EPSW3060 (UNQ3060) mRNA, complete cds	701	701	100%	0.0	100%	U G
NM_178134.2	Homo sapiens cytochrome P450, family 4, subfamily Z, polypeptide 1 (CYP4Z1), mRNA	701	701	100%	0.0	100%	U E G
XM_001133951.1	PREDICTED: Homo sapiens cytochrome P450, family 4, subfamily Z, polypeptide 1 (CYP4Z1), mRNA	695	695	100%	0.0	99%	G
AY262057.1	Homo sapiens cytochrome P450 (CYP4Z2P) pseudogene mRNA, complete sequence	645	645	100%	0.0	97%	U G
NR_002788.1	Homo sapiens cytochrome P450 4Z2 pseudogene (CYP4Z2P) on chromosome 1 >dbj|AK097373.1| Homo sapiens cDNA FLJ40054 fis, clone TBAES2000315, weakly similar to CYTOCHROME P450 4A1 (EC 1.14.15.3)	645	645	100%	0.0	97%	E G
AY696295.1	Homo sapiens cytochrome P450 (CYP4Z2P) mRNA, complete cds, alternatively spliced	460	646	99%	1e-126	98%	U G
XR_023310.1	PREDICTED: Pan troglodytes similar to cytochrome P450 (LOC456834), mRNA	398	398	59%	1e-107	98%	G
XR_017801.1	PREDICTED: Homo sapiens cytochrome P450 4Z2 pseudogene (CYP4Z2P), misc RNA	374	374	59%	2e-100	96%	G
XM_001175282.1	PREDICTED: Pan troglodytes hypothetical protein LOC750893 (LOC750893), partial mRNA	285	285	40%	9e-74	100%	G
XM_001147911.1	PREDICTED: Pan troglodytes hypothetical protein LOC743794 (LOC743794), partial mRNA	285	285	40%	9e-74	100%	G
AL450996.2	Human DNA sequence from clone RP11-184J23 on chromosome 1 Contains the gene for likely ortholog of rat cytochrome P450 4X1 (CYP4X1), the 5'	285	285	40%	9e-74	100%	

	end of the gene for cytochrome P450 4Z1 (CYP4Z1) and a tubulin alpha pseudogene, complete sequence					
AL731892.6	Human DNA sequence from clone RP11-346M5 on chromosome 1 Contains the 5' end of a cytochrome P450 4Z1 (CYP4Z1) pseudogene, a tubulin alpha pseudogene, the CYP4A11 gene for cytochrome P450 family 4 subfamily A polypeptide 11, complete sequence ·	285	285	40%	9e-74	100%
AL356793.19	Human DNA sequence from clone RP4-732G19 on chromosome 1p31.3-32.3 Contains the 3' end of the CYP4B1 gene for cytochrome P450 family 4 subfamily B polypeptide 1 and the 3' end of a cytochrome P450 4Z1 (CYP4Z1) pseudogene, complete sequence	285	651	99%	9e-74	100%
AL135960.1	Human DNA sequence from clone RP1-18D14 on chromosome 1 Contains the 3' end of the gene for cytochrome P450 4Z1 (CYP4Z1), the gene for a novel protein similar to cytochrome P450 family 4 subfamily A polypeptide 11 (CYP4A11) (LOC284541), a NADH dehydrogenase 1 mitochondrial pseudogene, three novel genes, the gene for membrane-associated protein 17 (MAP17), the TAL1 gene for T-cell acute lymphocytic leukemia 1, the 3' end of the SIL gene for TAL1 (SCL) interrupting locus and a CpG island, complete sequence	285	706	100%	9e-74	100% E
AJ131016.1	Homo sapiens SCL gene locus	285	706	100%	9e-74	100% E
AC203188.3	Rhesus Macaque BAC CH250-61I12 () complete sequence	202	202	31%	9e-49	96%